



SEQUENCE LISTING

<110> Keith D. Allen

<120> CXCR6 Chemokine Receptor Gene

Disruptions, Compositons and Methods Related Thereto

<130> R-976

<140> US 10/603,141

<141> 2003-06-24

<150> US 60/391,185

<151> 2002-06-24

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1251

<212> DNA

<213> Mus musculus

<400> 1

```
gaattcggca cgagggcaga ccttttagtga gcacacttca ctctggaaca aagctactgg 60
gcttctcttc tgatgccatg gatgatgggc atcaagagtc agctctgtac gatgggcact 120
acgagggaga tttctggctc ttcaacaatt ccagtgataa cagccaggag aacaaacgct 180
tcctaaagt caaggaggct tttttgccct gtgtgtacct ggtagtgttt gtctttggac 240
tgctaggaaa ctccctgggt ctgattatat acattttcta ccagaagctg aggactctga 300
cagatgtgtt tctgctgaac ttgcccctgg ctgacctggt gtttgtctgt actctgccct 360
tttgggccta tgcaggcacc tatgagtggg tctttggcac agtcatgtgc aaaactcttc 420
gaggcatgta tacaatgaac ttctacgtgt ccatgctcac tctcacctgc atcacagtgg 480
atcgtttcat tgtagtggtc caggctacca aggccttcaa ccggcaggct aagtgggaaga 540
tctggggcca agtcatttgc ttgctcattt ggggtggtct cctggttggt tctttgccac 600
agatcatcta tggccatggt caagataattg acaagcttat ctgtcagtac cacagtgagg 660
agatatccac tatggttctt gttatacaga tgactctggg gttcttctctg ccattgctca 720
ctatgattct gtgctactca ggcattatca agaccttgct tcatgctcga aacttccaga 780
agcacaaatc tctaaagatc atcttccttg tagtggctgt gttcctgctg acccagacac 840
ccttcaacct tgccatgtta atccaaagta caagctggga gtactataacc ataaccagct 900
ttaagtatgc catcgtagtg acagaggcta tagcatactt tcgggcttgc cttaaccctg 960
tactttatgc ctttggttggc ttaaagttcc ggaagaacgt ctggaaactt atgaaggata 1020
tcggctgcct ctctcacctg ggagtctcaa gtcaatggaa gtcttctgag gacagttcca 1080
agacttggtc tgccctccac aatgtagaga ccaccagtat gttccaattg tagtaggcct 1140
tgccacactt agagaagtta ataacagaat tctaggagca tggctgtatc atttggatgc 1200
aacaagaaaa gctttgctta tagcatgtgg agtatcatgg agaagcctga c 1251
```

<210> 2

<211> 348

<212> PRT

<213> Mus musculus

<400> 2

```
Gly His Gln Glu Ser Ala Leu Tyr Asp Gly His Tyr Glu Gly Asp Phe
1 5 10 15
```

Trp Leu Phe Asn Asn Ser Ser Asp Asn Ser Gln Glu Asn Lys Arg Phe
 20 25 30
 Leu Lys Phe Lys Glu Val Phe Leu Pro Cys Val Tyr Leu Val Val Phe
 35 40 45
 Val Phe Gly Leu Leu Gly Asn Ser Leu Val Leu Ile Ile Tyr Ile Phe
 50 55 60
 Tyr Gln Lys Leu Arg Thr Leu Thr Asp Val Phe Leu Leu Asn Leu Pro
 65 70 75 80
 Leu Ala Asp Leu Val Phe Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala
 85 90 95
 Gly Thr Tyr Glu Trp Val Phe Gly Thr Val Met Cys Lys Thr Leu Arg
 100 105 110
 Gly Met Tyr Thr Met Asn Phe Tyr Val Ser Met Leu Thr Leu Thr Cys
 115 120 125
 Ile Thr Val Asp Arg Phe Ile Val Val Val Gln Ala Thr Lys Ala Phe
 130 135 140
 Asn Arg Gln Ala Lys Trp Lys Ile Trp Gly Gln Val Ile Cys Leu Leu
 145 150 155 160
 Ile Trp Val Val Ser Leu Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly
 165 170 175
 His Val Gln Asp Ile Asp Lys Leu Ile Cys Gln Tyr His Ser Glu Glu
 180 185 190
 Ile Ser Thr Met Val Leu Val Ile Gln Met Thr Leu Gly Phe Phe Leu
 195 200 205
 Pro Leu Leu Thr Met Ile Leu Cys Tyr Ser Gly Ile Ile Lys Thr Leu
 210 215 220
 Leu His Ala Arg Asn Phe Gln Lys His Lys Ser Leu Lys Ile Ile Phe
 225 230 235 240
 Leu Val Val Ala Val Phe Leu Leu Thr Gln Thr Pro Phe Asn Leu Ala
 245 250 255
 Met Leu Ile Gln Ser Thr Ser Trp Glu Tyr Tyr Thr Ile Thr Ser Phe
 260 265 270
 Lys Tyr Ala Ile Val Val Thr Glu Ala Ile Ala Tyr Phe Arg Ala Cys
 275 280 285
 Leu Asn Pro Val Leu Tyr Ala Phe Val Gly Leu Lys Phe Arg Lys Asn
 290 295 300
 Val Trp Lys Leu Met Lys Asp Ile Gly Cys Leu Ser His Leu Gly Val
 305 310 315 320
 Ser Ser Gln Trp Lys Ser Ser Glu Asp Ser Ser Lys Thr Cys Ser Ala
 325 330 335
 Ser His Asn Val Glu Thr Thr Ser Met Phe Gln Leu
 340 345

<210> 3
 <211> 200
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Targeting Vector

<400> 3
 aaagacagtg ggaagaaaga atgtcactca gacataccca aatataactt ttaggttctg 60
 actcacagat gtttgcccca acagatgccca tggatgatgg gcatcaagag tcagctctgt 120
 acgatgggca ctacgaggga gatttctggc tcttcaacaa ttccagtgat aacagccagg 180
 agaacaaacg cttcctaaag 200

<210> 4
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting Vector

<400> 4
caggcaccta tgagtgggtc ttggcacag tcatgtgcaa aactcttcga ggcattgata 60
caatgaactt ctacgtgtcc atgtcactc tcacctgcat cacagtggat cgtttcattg 120
tagtgggtcca ggctaccaag gccttcaacc ggcaggctaa gtggaagatc tggggccaag 180
tcatttgctt gctcatttgg 200